

28758
SEQUENCE LISTING

<110> Gertler, Arieh
Krishna, Radha G.

<120> LEPTIN BINDING DOMAIN COMPOSITIONS AND METHODS THERETO

<130> 28758.1

<160> 8

<170> PatentIn version 3.2

<210> 1

<211> 630

<212> DNA

<213> human leptin receptor binding domain

<220>

<221> CDS

<222> (1)..(630)

<220>

<221> misc_feature

<222> (6)..(6)

<223> n is a, c, g, or t

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tta	act	aaa	atg	act	tgc	aga	tgg	tca	acc	agt	aca	atc	cag	tca	ctt	96
Leu	Thr	Lys	Met	Thr	Cys	Arg	Trp	Ser	Thr	Ser	Thr	Ile	Gln	Ser	Leu	
			20					25					30			

gcg	gaa	agc	act	ttg	caa	ttg	agg	tat	cat	agg	agc	agc	ctt	tac	tgt	144
Ala	Glu	Ser	Thr	Leu	Gln	Leu	Arg	Tyr	His	Arg	Ser	Ser	Leu	Tyr	Cys	
		35					40					45				

tct	gat	att	cca	tct	att	cat	ccc	ata	tct	gag	ccc	aaa	gat	tgc	tat	192
Ser	Asp	Ile	Pro	Ser	Ile	His	Pro	Ile	Ser	Glu	Pro	Lys	Asp	Cys	Tyr	
	50					55					60					

ttg	cag	agt	gat	ggg	ttt	tat	gaa	tgc	att	ttc	cag	cca	atc	ttc	cta	240
Leu	Gln	Ser	Asp	Gly	Phe	Tyr	Glu	Cys	Ile	Phe	Gln	Pro	Ile	Phe	Leu	
65					70					75					80	

tta	tct	ggc	tac	aca	atg	tgg	att	agg	atc	aat	cac	tct	cta	ggg	tca	288
Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Arg	Ile	Asn	His	Ser	Leu	Gly	Ser	
				85					90					95		

ctt	gac	tct	cca	cca	aca	tgt	gtc	ctt	cct	gat	tct	gtg	gtg	aag	cca	336
Leu	Asp	Ser	Pro	Pro	Thr	Cys	Val	Leu	Pro	Asp	Ser	Val	Val	Lys	Pro	
			100					105					110			

ctg	cct	cca	tcc	agt	gtg	aaa	gca	gaa	att	act	ata	aac	att	gga	tta	384
Leu	Pro	Pro	Ser	Ser	Val	Lys	Ala	Glu	Ile	Thr	Ile	Asn	Ile	Gly	Leu	
		115					120					125				

ttg	aaa	ata	tct	tgg	gaa	aag	cca	gtc	ttt	cca	gag	aat	aac	ctt	caa	432
Leu	Lys	Ile	Ser	Trp	Glu	Lys	Pro	Val	Phe	Pro	Glu	Asn	Asn	Leu	Gln	

130	135	28758 140	
ttc cag att cgc tat ggt tta agt gga aaa gaa gta caa tgg aag atg Phe Gln Ile Arg Tyr Gly Leu Ser Gly Lys Glu Val Gln Trp Lys Met 145 150 155 160			480
tat gag gtt tat gat gca aaa tca aaa tct gtc agt ctc cca gtt cca Tyr Glu Val Tyr Asp Ala Lys Ser Lys Ser Val Ser Leu Pro Val Pro 165 170 175			528
gac ttg tgt gca gtc tat gct gtt cag gtg cgc tgt aag agg cta gat Asp Leu Cys Ala Val Tyr Ala Val Gln Val Arg Cys Lys Arg Leu Asp 180 185 190			576
gga ctg gga tat tgg agt aat tgg agc aat cca gcc tac aca gtt gtc Gly Leu Gly Tyr Trp Ser Asn Trp Ser Asn Pro Ala Tyr Thr Val Val 195 200 205			624
atg gat Met Asp 210			630

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 <213> human leptin receptor binding domain

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Leu Thr Lys Met Thr Cys Arg Trp Ser Thr Ser Thr Ile Gln Ser Leu
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Ala Glu Ser Thr Leu Gln Leu Arg Tyr His Arg Ser Ser Leu Tyr Cys
35 40 45

Ser Asp Ile Pro Ser Ile His Pro Ile Ser Glu Pro Lys Asp Cys Tyr
50 55 60

Leu Gln Ser Asp Gly Phe Tyr Glu Cys Ile Phe Gln Pro Ile Phe Leu
65 70 75 80

Leu Ser Gly Tyr Thr Met Trp Ile Arg Ile Asn His Ser Leu Gly Ser
85 90 95

Leu Asp Ser Pro Pro Thr Cys Val Leu Pro Asp Ser Val Val Lys Pro
100 105 110

Leu Pro Pro Ser Ser Val Lys Ala Glu Ile Thr Ile Asn Ile Gly Leu
115 120 125

Leu Lys Ile Ser Trp Glu Lys Pro Val Phe Pro Glu Asn Asn Leu Gln
Page 2

<220>
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 <222> (3)..(3)
 <223> Xaa can be any naturally occurring amino acid

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Trp Ser Xaa Trp Ser
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<210> 7
 <211> 627
 <212> DNA
 <213> chicken leptin receptor binding domain

<220>
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 <222> (1)..(627)

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 tta act aaa atg act tgc aga tgg tct gca aac cca aac gca ttg ctc 96
 Leu Thr Lys Met Thr Cys Arg Trp Ser Ala Asn Pro Asn Ala Leu Leu
 20 25 30
 ttg ggg agt tcc ttg cag tta aga tac cac agg agc aaa att tat tgt 144
 Leu Gly Ser Ser Leu Gln Leu Arg Tyr His Arg Ser Lys Ile Tyr Cys
 35 40 45
 tct aac ttt cca agt act cct cca gaa tca gag gtg aaa gaa tgc cat 192
 Ser Asn Phe Pro Ser Thr Pro Pro Glu Ser Glu Val Lys Glu Cys His
 50 55 60
 ttc cag agg aat cat tct tat gag tgc aca ttt cag cct gtt ttt ctt 240
 Phe Gln Arg Asn His Ser Tyr Glu Cys Thr Phe Gln Pro Val Phe Leu
 65 70 75 80
 tta tct gga tat acc atg tgg att gag ctt aag cac tcg ctg gga aca 288
 Leu Ser Gly Tyr Thr Met Trp Ile Glu Leu Lys His Ser Leu Gly Thr
 85 90 95
 ctt gaa tcc tca cca act tgt gtc gtt cca gca gat gtg gtg aag cca 336
 Leu Glu Ser Ser Pro Thr Cys Val Val Pro Ala Asp Val Val Lys Pro
 100 105 110
 ctg cct ccc tcc aac att aaa gca gag atc acc aga aac gat ggg ctg 384
 Leu Pro Pro Ser Asn Ile Lys Ala Glu Ile Thr Arg Asn Asp Gly Leu
 115 120 125
 ctg aac gtg agc tgg aca aac ccc gtg ttt aca aat gat gac ctt aag 432
 Leu Asn Val Ser Trp Thr Asn Pro Val Phe Thr Asn Asp Asp Leu Lys
 130 135 140

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ttt	cag	atc	cgg	tac	gca	gtg	aac	agg	gaa	gaa	ctc	aca	tgg	gag	ctg	480
Phe	Gln	Ile	Arg	Tyr	Ala	Val	Asn	Arg	Glu	Glu	Leu	Thr	Trp	Glu	Leu	
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tat	gaa	gtt	cta	agc	gta	cca	aca	aga	tca	gct	gtg	ata	gaa	gtg	caa	528
Tyr	Glu	Val	Leu	Ser	Val	Pro	Thr	Arg	Ser	Ala	Val	Ile	Glu	Val	Gln	
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ctt	tgt	gtt	gaa	tat	att	gtt	cag	atc	cgc	tgc	aga	gcc	ctg	gat	ggc	576
Leu	Cys	Val	Glu	Tyr	Ile	Val	Gln	Ile	Arg	Cys	Arg	Ala	Leu	Asp	Gly	
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tta	ggc	tac	tgg	agc	aac	tgg	agc	aga	tca	gcc	tat	gca	gct	gta	aaa	624
Leu	Gly	Tyr	Trp	Ser	Asn	Trp	Ser	Arg	Ser	Ala	Tyr	Ala	Ala	Val	Lys	
		195					200					205				
gat																627
Asp																

<210> 8
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Met	Ala	Val	Asp	Val	Asn	Ile	Asn	Ile	Lys	Cys	Glu	Thr	Asp	Gly	Tyr	
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			20					25					30			
Leu	Gly	Ser	Ser	Leu	Gln	Leu	Arg	Tyr	His	Arg	Ser	Lys	Ile	Tyr	Cys	
		35					40					45				
Ser	Asn	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Ser	Glu	Val	Lys	Glu	Cys	His	
	50					55					60					
Phe	Gln	Arg	Asn	His	Ser	Tyr	Glu	Cys	Thr	Phe	Gln	Pro	Val	Phe	Leu	
65					70					75					80	
Leu	Ser	Gly	Tyr	Thr	Met	Trp	Ile	Glu	Leu	Lys	His	Ser	Leu	Gly	Thr	
				85					90					95		
Leu	Glu	Ser	Ser	Pro	Thr	Cys	Val	Val	Pro	Ala	Asp	Val	Val	Lys	Pro	
			100					105					110			
Leu	Pro	Pro	Ser	Asn	Ile	Lys	Ala	Glu	Ile	Thr	Arg	Asn	Asp	Gly	Leu	
		115					120					125				
Leu	Asn	Val	Ser	Trp	Thr	Asn	Pro	Val	Phe	Thr	Asn	Asp	Asp	Leu	Lys	
	130					135					140					

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Phe Gln Ile Arg Tyr Ala Val Asn Arg Glu Glu Leu Thr Trp Glu Leu
145 150 155 160

Tyr Glu Val Leu Ser Val Pro Thr Arg Ser Ala Val Ile Glu Val Gln
165 170 175

Leu Cys Val Glu Tyr Ile Val Gln Ile Arg Cys Arg Ala Leu Asp Gly
180 185 190

Leu Gly Tyr Trp Ser Asn Trp Ser Arg Ser Ala Tyr Ala Ala Val Lys
195 200 205

Asp